THE CLAIMS

What is claimed is:

1. A parallel electrophoresis system having a plurality of separation lanes, a detector and a processor connected to the detector, wherein light intensity is received at the detector from at least two different separation lanes, and processed using at least two different calibration matrices.

2. A method of calibrating a detection system in an electrophoresis apparatus comprising of at least one separation lane, the detection system configured to sense a spectrum of light intensities over a number *m* wavelength channels from said at least one separation lane, the method comprising:

detecting at least one spectrum of light intensities for each of a plurality of samples;

clustering the detected spectra of light intensities into a number *n* categories by using predetermined clustering criteria; and

creating a calibration matrix from the clusters.

3. The method according to claim 2, wherein detected spectra of at least some samples are discarded prior to the clustering step.

4. The method according to claim 2, wherein a calibration matrix is determined for each of a corresponding plurality of separation lanes.

5. The method according to claim 4, wherein a total of at least 96 calibration matrices are generated, one for each of a corresponding separation lane.

6. An electrophoresis separation apparatus having at least one separation lane, a detector, and a processor, wherein the apparatus is configured to:

detect at least one spectrum of light intensities for each of a plurality of samples;

cluster the detected sets of light intensities into a number *n* categories by using predetermined clustering criteria; and

create a calibration matrix from the cluster.

7. The electrophoresis separation apparatus according to claim 6, wherein the apparatus is configured to discard the spectra of at least some samples prior to the clustering step.

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8. A method of identifying nucleotides in an electrophoretically separated DNA sample which has been tagged with a chromophore, comprising:

displaying light intensities on a two dimensional time-wavelength plot; and

identifying nucleotides based upon the shape and position of said formations displayed on said plot.

9. An electrophoretic detection system for separating a sample containing therein a plurality of dye components, wherein the detection apparatus is configured to automatically determine the number of different dye components from spectra of the sample.

10. A method for automatically calibrating an electrophoretic separation apparatus having a plurality of separation lanes, the method comprising the steps of:

for each separation lane, detecting a plurality of sets of light intensities from a migrating sample, the light intensities in each set being collected in a total of R channels, where $R \geq 2$;

for each separation lane, isolating peaks in at least some of the plurality of sets of light intensities;

estimating a number of dyes M present in the migrating sample based on the isolated peaks, where $M \geq 2$; and

for each separation lane, calculating coefficients based on the distribution of light intensities in the channels of the isolated peaks, wherein the coefficients map detected light intensities from the R channels onto values reflective of the relative likelihood of each of the dyes being present.

11. A method according to claim 10, wherein the coefficients are arranged in the form of an R x M matrix.

12. A parallel electrophoresis system having a plurality of separation lanes for simultaneous separation of a sample in each of the separation lanes, a detector and a processor connected to the detector, wherein the processor is configured to simultaneously process light detected from species tagged with dyes belonging to more than one dye set.

13. A method for automatically calibrating a separation apparatus, said method comprising the steps of:

sampling light emitted from species having a chromophore, the sampling being performed over a first number *m* of wavelength channels and a second number *n* of time intervals to thereby form a time-wavelength distribution wherein a total of *k* discrete species are represented by morphological formations in the said time-wavelength distribution;

isolating a total of *l* peaks from said formations, each peak corresponding to a discrete species;

clustering the *l* peaks into a number *j* classes based on at least one similarity criterion;

forming a total of *j* calibration vectors, each calibration vector representing one of said classes; and

forming a calibration matrix *A* comprising of the *j* calibration vectors.

14. The method of claim 13, wherein the method of isolating *l* peaks from the formations comprises of:

preprocessing the sample data in the time domain;

isolating a total of *p* peaks in the time domain; and

isolating a total *l* peaks from *p* peaks according to the width and spacing of said peaks in the time domain;

15. The method of claim 13, wherein the step of isolating peaks comprises employing morphological filters to identify peaks in the time-wavelength distribution.

16. The method of claim 13, wherein the step of isolating peaks comprises visually inspecting the time-wavelength distribution and selecting those peaks which are unconnected to other peaks.